



1200029-US2.ST25.txt  
SEQUENCE LISTING

<110> Soll, Dieter  
<120> GlutRNAGLN AMIDOTRANSFERASE - A NOVEL ESSENTIAL TRANSLATIONAL COMPONENT  
<130> 03818/1200029-US2  
<140> 10/661,399  
<141> 2003-09-12  
<150> 60/037,275  
<151> 1997-02-03  
<150> PCT/US98/01860  
<151> 1998-02-03  
<150> 09/355,622  
<151> 1999-09-23  
<160> 8  
<170> PatentIn version 3.2  
<210> 1  
<211> 3495  
<212> DNA  
<213> Bacillus subtilis  
  
<220>  
<221> misc\_feature  
<222> (2330)..(2330)  
<223> n is a, c, g, or t  
  
<220>  
<221> misc\_feature  
<222> (2365)..(2365)  
<223> n is a, c, g, or t  
  
<400> 1  
gaattcgatc ctgtctcaag gcgttttgtt gctttaaagg gcttgttttt gatatgatca 60  
gtattatatg acttaacgga gaaatatgtg gaggtggatc atatgtcacg aatttcaata 120  
gaagaagtaa agcacgttgc gcaccttgca agacttgcca ttactgaaga agaagcaaaa 180  
atgttcactg aacagctcga cagtatcatt tcatttgccg aggagcttaa tgaggttaac 240  
acagacaatg tggagcctac aactcacgtg ctgaaaatga aaaatgtcat gagagaagat 300  
gaagcgggta aaggtcttcc gggttgaggat gtcatgaaaa atgcgcctga ccataaagac 360  
ggctatattc gtgtgccatc aattctggac taaaggaggg acacaagaat gtcattattt 420  
gatcataaaa tcacagaatt aaaacagctc atacataaaa aagagattaa gatttctgat 480  
ctggttgatg aatcttataa acgcatccaa gcggttgatg ataagggtaca agcctttttg 540  
gcattagatg aagaaagagc gcgcgcatac gcgaaggagc ttgatgaggc gggtgacggc 600  
cgttctgagc acggtcttct tttcggtatg cccatcggcg taaaagataa tatcgtaaca 660

## 1200029-US2.ST25.txt

aaagggctgc gcacaacatg ctccagcaaa attctcga aa actttgatcc gatttacgat	720
gctactgtcg ttcagcgcct tcaagacgct gaagcgggtca caatcgga aa actgaacatg	780
gacgaattcg ccatgggggtc atctacagaa aactcagctt acaagctgac gaaaaaccct	840
tggaacctgg atacagttcc cggcgggttca agcggcggat ctgcagctgc ggttgctgcg	900
ggagaagtgc cgttttctct tggatctgac acaggcggct ccatccgtca gccggcatct	960
ttctgcggcg ttgtcggatt aaaacctaca tacggacgtg tatctcgta cggcctgggtc	1020
gcatttgctg cttcattgga ccaaatcgga ccgattacac gtacgggtga ggataacgcg	1080
tttttacttc aagcgatttc cggcgtagac aaaatggact ctacgagtgc aaatgtggac	1140
gtgcctgatt ttctttcttc attaaactggc gacatcaaag gactgaaaat cgccgtttccg	1200
aaagaatacc ttggtgaagg tgtcggcaaa gaagcgagag aatctgtctt ggcagcgtg	1260
aaagtccttg aaggtctcgg cgctacatgg gaagaagtgt ctcttcgcga cagtaaatac	1320
gcgcttgcca catattacct gctgtcatct tctgaagcgt cagcgaacct tgcacgcttt	1380
gacggcatcc gctacggcta ccgcacagac aacgcggata acctgatcga cttttacaag	1440
caaacgcgcg ctgaagggtt cggaatgaa gtcaaacgcc gcatcatgct cggaacgttt	1500
gctttaagct caggctacta cgatgcgtac taca aaaaag cgcaaaaagt gcgtacgttg	1560
attaagaagg atttcgagga cgtatttgaa aaatatgatg ttattgttgg accgactaca	1620
ccgacacctg cgtttaaaat cggtgaaaac acgaaggatc cgctcacaat gtacgcaaac	1680
gatatcttaa cgattccggt caaccttgcg gcgtaccggg aatcaggtgc catgcggtta	1740
gcagacggac ttccgctcgg cctgcaaadc atcggaaaac actttgatga agcactgtat	1800
accgcgttgc tcatgcattt gaacaagcaa cagaccatca taaagcaaaa cctgaactgt	1860
aaggggtgaa aagaattgaa ctttgaaacg gtaatcggac ttgaagtcca cgttgagtta	1920
aaaacaaaat caaaaatttt ctcaagctct ccaacgccat tcggcgcgga ggcgaatacg	1980
cagacaagcg ttattgacct cggatatccg ggcgtcctgc ctgttctgaa caaagaagcc	2040
gttgaaattcg caatgaaagc cgctatggcg ctcaactgtg agatcgcaac ggatacgaag	2100
tttgaccgca aaaactattt ctatcctgac aaccgaaaag cgtatcagat ttctcaattt	2160
gataagccaa tcggcgaaaa cggctggatc gaaattgaag tcggcggcaa aacaaaacgc	2220
atcggcatca cgcgccttca tcttgaagag gatgccggaa aactgacgca tacgggcgac	2280
ggctattctc ttgttgactt caaccgtcaa ggaacgccgc ttgttgagtn cgtatcagag	2340
ccggacatcc gcacgccgga agaancgtac gcatactttg aaaagctgaa atccatcatc	2400
caatatacag gcgtttctga ctgtaaaatg gaagaaggct cacttcgctg tgacgccaat	2460
atctctcttc gtccgatcgg ccaagaggaa ttcggcacia aaacagaatt gaaaaacttg	2520

1200029-US2.ST25.txt

aactcctttg cgtttgttca aaaaggcctt gagcatgaag aaaaacgcca ggagcaggtt 2580  
cttctttccg gcttcttcat ccagcaagaa actcgccgtt atgatgaagc aacgaagaaa 2640  
accattctta tgcgtgtcaa agagggatct gacgactacc gttactttcc agagccagat 2700  
ctagtcgagc tctacattga tgatgaatgg aaggaacgcg taaaagcaag cattcctgag 2760  
cttccggatg agcgccgcaa gcgttatatc gaagagcttg gcttcgctgc atatgacgca 2820  
atggttctga cgctgacaaa agaaatggct gatttcttcg aagaaaccgt tcaaaaaggc 2880  
gctgaagcta aacaagcgtc taactggctg atgggtgaag tgtcagctta cctaaacgca 2940  
gaacaaaaag agcttgccga tgttgccctg acacctgaag gccttgccgg catgatcaaa 3000  
ttgattgaaa aaggaaccat ttcttctaag atcgcaaga aagtgtttaa agaattgatt 3060  
gaaaaaggcg gcgacgctga gaagattgtg aaagagaaaag gccttgttca gatttctgac 3120  
gaaggcgtgc ttctgaagct tgtcactgag gcgcttgaca acaatcctca atcaatcgaa 3180  
gactttaaaa acggaaga cgcgcgcatc ggcttcctag tcggacagat tatgaaagcg 3240  
tccaaaggac aagccaaccc gccgatggct aacaaaattc tgcttgaaga aattaaaaaa 3300  
cgctaataaa aaagcagccc ttagaggctg ctttttttat ggtcaaattg agataaagac 3360  
aagatgaggg cccgaagcct ttcaacttct ttgtcgttgg ttccggccaa attggacagc 3420  
atgcctttat aatcggcttg cgcggtttat cctgagtcaa ttcttcctcg ataagataag 3480  
tgacacggtg atatc 3495

<210> 2  
<211> 1155  
<212> PRT  
<213> Bacillus subtilis

<220>  
<221> misc\_feature  
<222> (774)..(774)  
<223> Xaa is Phe, Ser, Tyr, or Cys

<220>  
<221> misc\_feature  
<222> (786)..(786)  
<223> Xaa is Ser, Pro, Thr, or Ala

<400> 2

Glu Phe Asp Pro Val Ser Arg Arg Phe Val Ala Leu Lys Gly Leu Phe  
1 5 10 15

Leu Ile Ser Val Leu Tyr Asp Leu Thr Glu Lys Tyr Val Glu Val Asp  
20 25 30

His Met Ser Arg Ile Ser Ile Glu Glu Val Lys His Val Ala His Leu  
35 40 45

1200029-US2.ST25.txt

Ala Arg Leu Ala Ile Thr Glu Glu Glu Ala Lys Met Phe Thr Glu Gln  
50 55 60

Leu Asp Ser Ile Ile Ser Phe Ala Glu Glu Leu Asn Glu Val Asn Thr  
65 70 75 80

Asp Asn Val Glu Pro Thr Thr His Val Leu Lys Met Lys Asn Val Met  
85 90 95

Arg Glu Asp Glu Ala Gly Lys Gly Leu Pro Val Glu Asp Val Met Lys  
100 105 110

Asn Ala Pro Asp His Lys Asp Gly Tyr Ile Arg Val Pro Ser Ile Leu  
115 120 125

Asp Arg Arg Asp Thr Arg Met Ser Leu Phe Asp His Lys Ile Thr Glu  
130 135 140

Leu Lys Gln Leu Ile His Lys Lys Glu Ile Lys Ile Ser Asp Leu Val  
145 150 155 160

Asp Glu Ser Tyr Lys Arg Ile Gln Ala Val Asp Asp Lys Val Gln Ala  
165 170 175

Phe Leu Ala Leu Asp Glu Glu Arg Ala Arg Ala Tyr Ala Lys Glu Leu  
180 185 190

Asp Glu Ala Val Asp Gly Arg Ser Glu His Gly Leu Leu Phe Gly Met  
195 200 205

Pro Ile Gly Val Lys Asp Asn Ile Val Thr Lys Gly Leu Arg Thr Thr  
210 215 220

Cys Ser Ser Lys Ile Leu Glu Asn Phe Asp Pro Ile Tyr Asp Ala Thr  
225 230 235 240

Val Val Gln Arg Leu Gln Asp Ala Glu Ala Val Thr Ile Gly Lys Leu  
245 250 255

Asn Met Asp Glu Phe Ala Met Gly Ser Ser Thr Glu Asn Ser Ala Tyr  
260 265 270

Lys Leu Thr Lys Asn Pro Trp Asn Leu Asp Thr Val Pro Gly Gly Ser  
275 280 285

Ser Gly Gly Ser Ala Ala Ala Val Ala Ala Gly Glu Val Pro Phe Ser  
Page 4

290

295

Leu Gly Ser Asp Thr Gly Gly Ser Ile Arg Gln Pro Ala Ser Phe Cys  
305 310 315 320

Gly Val Val Gly Leu Lys Pro Thr Tyr Gly Arg Val Ser Arg Tyr Gly  
325 330 335

Leu Val Ala Phe Ala Ser Ser Leu Asp Gln Ile Gly Pro Ile Thr Arg  
340 345 350

Thr Val Glu Asp Asn Ala Phe Leu Leu Gln Ala Ile Ser Gly Val Asp  
355 360 365

Lys Met Asp Ser Thr Ser Ala Asn Val Asp Val Pro Asp Phe Leu Ser  
370 375 380

Ser Leu Thr Gly Asp Ile Lys Gly Leu Lys Ile Ala Val Pro Lys Glu  
385 390 395 400

Tyr Leu Gly Glu Gly Val Gly Lys Glu Ala Arg Glu Ser Val Leu Ala  
405 410 415

Ala Leu Lys Val Leu Glu Gly Leu Gly Ala Thr Trp Glu Glu Val Ser  
420 425 430

Leu Pro His Ser Lys Tyr Ala Leu Ala Thr Tyr Tyr Leu Leu Ser Ser  
435 440 445

Ser Glu Ala Ser Ala Asn Leu Ala Arg Phe Asp Gly Ile Arg Tyr Gly  
450 455 460

Tyr Arg Thr Asp Asn Ala Asp Asn Leu Ile Asp Leu Tyr Lys Gln Thr  
465 470 475 480

Arg Ala Glu Gly Phe Gly Asn Glu Val Lys Arg Arg Ile Met Leu Gly  
485 490 495

Thr Phe Ala Leu Ser Ser Gly Tyr Tyr Asp Ala Tyr Tyr Lys Lys Ala  
500 505 510

Gln Lys Val Arg Thr Leu Ile Lys Lys Asp Phe Glu Asp Val Phe Glu  
515 520 525

Lys Tyr Asp Val Ile Val Gly Pro Thr Thr Pro Thr Pro Ala Phe Lys  
530 535 540

1200029-US2.ST25.txt

Ile Gly Glu Asn Thr Lys Asp Pro Leu Thr Met Tyr Ala Asn Asp Ile  
545 550 555 560

Leu Thr Ile Pro Val Asn Leu Ala Ala Tyr Arg Glu Ser Gly Ala Met  
565 570 575

Arg Leu Ala Asp Gly Leu Pro Leu Gly Leu Gln Ile Ile Gly Lys His  
580 585 590

Phe Asp Glu Ala Leu Tyr Thr Ala Leu Leu Met His Leu Asn Lys Gln  
595 600 605

Gln Thr Ile Ile Lys Gln Asn Leu Asn Cys Lys Gly Lys Glu Leu Asn  
610 615 620

Phe Glu Thr Val Ile Gly Leu Glu Val His Val Glu Leu Lys Thr Lys  
625 630 635 640

Ser Lys Ile Phe Ser Ser Ser Pro Thr Pro Phe Gly Ala Glu Ala Asn  
645 650 655

Thr Gln Thr Ser Val Ile Asp Leu Gly Tyr Pro Gly Val Leu Pro Val  
660 665 670

Leu Asn Lys Glu Ala Val Glu Phe Ala Met Lys Ala Ala Met Ala Leu  
675 680 685

Asn Cys Glu Ile Ala Thr Asp Thr Lys Phe Asp Arg Lys Asn Tyr Phe  
690 695 700

Tyr Pro Asp Asn Pro Lys Ala Tyr Gln Ile Ser Gln Phe Asp Lys Pro  
705 710 715 720

Ile Gly Glu Asn Gly Trp Ile Glu Ile Glu Val Gly Gly Lys Thr Lys  
725 730 735

Arg Ile Gly Ile Thr Arg Leu His Leu Glu Glu Asp Ala Gly Lys Leu  
740 745 750

Thr His Thr Gly Asp Gly Tyr Ser Leu Val Asp Phe Asn Arg Gln Gly  
755 760 765

Thr Pro Leu Val Glu Xaa Val Ser Glu Pro Asp Ile Arg Thr Pro Glu  
770 775 780

Glu Xaa Tyr Ala Tyr Leu Glu Lys Leu Lys Ser Ile Ile Gln Tyr Thr  
785 790 795 800

1200029-US2.ST25.txt

Gly Val Ser Asp Cys Lys Met Glu Glu Gly Ser Leu Arg Cys Asp Ala  
805 810 815

Asn Ile Ser Leu Arg Pro Ile Gly Gln Glu Glu Phe Gly Thr Lys Thr  
820 825 830

Glu Leu Lys Asn Leu Asn Ser Phe Ala Phe Val Gln Lys Gly Leu Glu  
835 840 845

His Glu Glu Lys Arg Gln Glu Gln Val Leu Leu Ser Gly Phe Phe Ile  
850 855 860

Gln Gln Glu Thr Arg Arg Tyr Asp Glu Ala Thr Lys Lys Thr Ile Leu  
865 870 875 880

Met Arg Val Lys Glu Gly Ser Asp Asp Tyr Arg Tyr Phe Pro Glu Pro  
885 890 895

Asp Leu Val Glu Leu Tyr Ile Asp Asp Glu Trp Lys Glu Arg Val Lys  
900 905 910

Ala Ser Ile Pro Glu Leu Pro Asp Glu Arg Arg Lys Arg Tyr Ile Glu  
915 920 925

Glu Leu Gly Phe Ala Ala Tyr Asp Ala Met Val Leu Thr Leu Thr Lys  
930 935 940

Glu Met Ala Asp Phe Phe Glu Glu Thr Val Gln Lys Gly Ala Glu Ala  
945 950 955 960

Lys Gln Ala Ser Asn Trp Leu Met Gly Glu Val Ser Ala Tyr Leu Asn  
965 970 975

Ala Glu Gln Lys Glu Leu Ala Asp Val Ala Leu Thr Pro Glu Gly Leu  
980 985 990

Ala Gly Met Ile Lys Leu Ile Glu Lys Gly Thr Ile Ser Ser Lys Ile  
995 1000 1005

Ala Lys Lys Val Phe Lys Glu Leu Ile Glu Lys Gly Gly Asp Ala  
1010 1015 1020

Glu Lys Ile Val Lys Glu Lys Gly Leu Val Gln Ile Ser Asp Glu  
1025 1030 1035

Gly Val Leu Leu Lys Leu Val Thr Glu Ala Leu Asp Asn Asn Pro  
1040 1045 1050

1200029-US2.ST25.txt

Gln Ser Ile Glu Asp Phe Lys Asn Gly Lys Asp Arg Ala Ile Gly  
1055 1060 1065

Phe Leu Val Gly Gln Ile Met Lys Ala Ser Lys Gly Gln Ala Asn  
1070 1075 1080

Pro Pro Met Val Asn Lys Ile Leu Leu Glu Glu Ile Lys Lys Arg  
1085 1090 1095

Lys Ser Ser Pro Arg Leu Leu Phe Leu Trp Ser Asn Asp Lys Asp  
1100 1105 1110

Lys Met Arg Ala Arg Ser Leu Ser Thr Ser Leu Ser Leu Val Pro  
1115 1120 1125

Ala Lys Leu Asp Ser Met Pro Leu Ser Ala Cys Ala Val Tyr Pro  
1130 1135 1140

Glu Ser Ile Leu Pro Arg Asp Lys His Gly Asp Ile  
1145 1150 1155

<210> 3  
<211> 1461  
<212> DNA  
<213> Bacillus subtilis

<220>  
<221> CDS  
<222> (1)..(1458)  
<223> Subunit A, corresponds to nucleotides 409-1869 of SEQ ID NO: 1

<400> 3  
atg tca tta ttt gat cat aaa atc aca gaa tta aaa cag ctc ata cat 48  
Met Ser Leu Phe Asp His Lys Ile Thr Glu Leu Lys Gln Leu Ile His  
1 5 10 15

aaa aaa gag att aag att tct gat ctg gtt gat gaa tct tat aaa cgc 96  
Lys Lys Glu Ile Lys Ile Ser Asp Leu Val Asp Glu Ser Tyr Lys Arg  
20 25 30

atc caa gcg gtt gat gat aag gta caa gcc ttt ttg gca tta gat gaa 144  
Ile Gln Ala Val Asp Asp Lys Val Gln Ala Phe Leu Ala Leu Asp Glu  
35 40 45

gaa aga gcg cgc gca tac gcg aag gag ctt gat gag gcg gtt gac ggc 192  
Glu Arg Ala Arg Ala Tyr Ala Lys Glu Leu Asp Glu Ala Val Asp Gly  
50 55 60

cgt tct gag cac ggt ctt ctt ttc ggt atg ccg atc ggc gta aaa gat 240  
Arg Ser Glu His Gly Leu Leu Phe Gly Met Pro Ile Gly Val Lys Asp  
65 70 75 80

aat atc gta aca aaa ggg ctg cgc aca aca tgc tcc agc aaa att ctc 288  
Page 8



## 1200029-US2.ST25.txt

Asn	Ile	Val	Thr	Lys	Gly	Leu	Arg	Thr	Thr	Cys	Ser	Ser	Lys	Ile	Leu		
				85				90						95			
gaa	aac	ttt	gat	ccg	att	tac	gat	gct	act	gtc	gtt	cag	cgc	ctt	caa	336	
Glu	Asn	Phe	Asp	Pro	Ile	Tyr	Asp	Ala	Thr	Val	Val	Gln	Arg	Leu	Gln		
			100					105					110				
gac	gct	gaa	gcg	gtc	aca	atc	gga	aaa	ctg	aac	atg	gac	gaa	ttc	gcc	384	
Asp	Ala	Glu	Ala	Val	Thr	Ile	Gly	Lys	Leu	Asn	Met	Asp	Glu	Phe	Ala		
			115				120					125					
atg	ggg	tca	tct	aca	gaa	aac	tca	gct	tac	aag	ctg	acg	aaa	aac	cct	432	
Met	Gly	Ser	Ser	Thr	Glu	Asn	Ser	Ala	Tyr	Lys	Leu	Thr	Lys	Asn	Pro		
	130					135					140						
tgg	aac	ctg	gat	aca	gtt	ccc	ggc	ggg	tca	agc	ggc	gga	tct	gca	gct	480	
Trp	Asn	Leu	Asp	Thr	Val	Pro	Gly	Gly	Ser	Ser	Gly	Gly	Ser	Ala	Ala		
	145				150					155					160		
gcg	gtt	gct	gcg	gga	gaa	gtt	ccg	ttt	tct	ctt	gga	tct	gac	aca	ggc	528	
Ala	Val	Ala	Ala	Gly	Glu	Val	Pro	Phe	Ser	Leu	Gly	Ser	Asp	Thr	Gly		
				165				170						175			
ggc	tcc	atc	cgt	cag	ccg	gca	tct	ttc	tgc	ggc	gtt	gtc	gga	tta	aaa	576	
Gly	Ser	Ile	Arg	Gln	Pro	Ala	Ser	Phe	Cys	Gly	Val	Val	Gly	Leu	Lys		
			180					185					190				
cct	aca	tac	gga	cgt	gta	tct	cgt	tac	ggc	ctg	gtc	gca	ttt	gcg	tct	624	
Pro	Thr	Tyr	Gly	Arg	Val	Ser	Arg	Tyr	Gly	Leu	Val	Ala	Phe	Ala	Ser		
			195				200					205					
tca	ttg	gac	caa	atc	gga	ccg	att	aca	cgt	acg	gtt	gag	gat	aac	gcg	672	
Ser	Leu	Asp	Gln	Ile	Gly	Pro	Ile	Thr	Arg	Thr	Val	Glu	Asp	Asn	Ala		
	210					215					220						
ttt	tta	ctt	caa	gcg	att	tcc	ggc	gta	gac	aaa	atg	gac	tct	acg	agt	720	
Phe	Leu	Leu	Gln	Ala	Ile	Ser	Gly	Val	Asp	Lys	Met	Asp	Ser	Thr	Ser		
					230					235					240		
gca	aat	gtg	gac	gtg	cct	gat	ttt	ctt	tct	tca	tta	act	ggc	gac	atc	768	
Ala	Asn	Val	Asp	Val	Pro	Asp	Phe	Leu	Ser	Ser	Leu	Thr	Gly	Asp	Ile		
				245					250					255			
aaa	gga	ctg	aaa	atc	gcc	gtt	ccg	aaa	gaa	tac	ctt	ggg	gaa	ggg	gtc	816	
Lys	Gly	Leu	Lys	Ile	Ala	Val	Pro	Lys	Glu	Tyr	Leu	Gly	Glu	Gly	Val		
			260					265					270				
ggc	aaa	gaa	gcg	aga	gaa	tct	gtc	ttg	gca	gcg	ctg	aaa	gtc	ctt	gaa	864	
Gly	Lys	Glu	Ala	Arg	Glu	Ser	Val	Leu	Ala	Ala	Leu	Lys	Val	Leu	Glu		
			275				280					285					
ggg	ctc	ggc	gct	aca	tgg	gaa	gaa	gtg	tct	ctt	ccg	cac	agt	aaa	tac	912	
Gly	Leu	Gly	Ala	Thr	Trp	Glu	Glu	Val	Ser	Leu	Pro	His	Ser	Lys	Tyr		
	290					295					300						
gcg	ctt	gcg	aca	tat	tac	ctg	ctg	tca	tct	tct	gaa	gcg	tca	gcg	aac	960	
Ala	Leu	Ala	Thr	Tyr	Tyr	Leu	Leu	Ser	Ser	Ser	Glu	Ala	Ser	Ala	Asn		
					310					315					320		
ctt	gca	cgc	ttt	gac	ggc	atc	cgc	tac	ggc	tac	cgc	aca	gac	aac	gcg	1008	
Leu	Ala	Arg	Phe	Asp	Gly	Ile	Arg	Tyr	Gly	Tyr	Arg	Thr	Asp	Asn	Ala		
				325					330					335			

1200029-US2.ST25.txt

gat aac ctg atc gac ctt tac aag	caa acg cgc gct gaa ggt ttc gga	1056
Asp Asn Leu Ile Asp Leu Tyr Lys	Gln Thr Arg Ala Glu Gly Phe Gly	
340	345 350	
aat gaa gtc aaa cgc cgc atc atg ctc gga acg ttt gct tta agc tca	1104	
Asn Glu Val Lys Arg Arg Ile Met Leu Gly Thr Phe Ala Leu Ser Ser		
355	360 365	
ggc tac tac gat gcg tac tac aaa aaa gcg caa aaa gtg cgt acg ttg	1152	
Gly Tyr Tyr Asp Ala Tyr Tyr Lys Lys Ala Gln Lys Val Arg Thr Leu		
370	375 380	
att aag aag gat ttc gag gac gta ttt gaa aaa tat gat gtt att gtt	1200	
Ile Lys Lys Asp Phe Glu Asp Val Phe Glu Lys Tyr Asp Val Ile Val		
385	390 395 400	
gga ccg act aca ccg aca cct gcg ttt aaa atc ggt gaa aac acg aag	1248	
Gly Pro Thr Thr Pro Thr Pro Ala Phe Lys Ile Gly Glu Asn Thr Lys		
405	410 415	
gat ccg ctc aca atg tac gca aac gat atc tta acg att ccg gtc aac	1296	
Asp Pro Leu Thr Met Tyr Ala Asn Asp Ile Leu Thr Ile Pro Val Asn		
420	425 430	
ctt gcg gcg tac cgg gaa tca ggt gcc atg cgg tta gca gac gga ctt	1344	
Leu Ala Ala Tyr Arg Glu Ser Gly Ala Met Arg Leu Ala Asp Gly Leu		
435	440 445	
ccg ctc ggc ctg caa atc atc gga aaa cac ttt gat gaa gca ctg tat	1392	
Pro Leu Gly Leu Gln Ile Ile Gly Lys His Phe Asp Glu Ala Leu Tyr		
450	455 460	
acc gcg ttg ctc atg cat ttg aac aag caa gag acc atc ata aag caa	1440	
Thr Ala Leu Leu Met His Leu Asn Lys Gln Glu Thr Ile Ile Lys Gln		
465	470 475 480	
aac ctg aac tgt aag ggg tga	1461	
Asn Leu Asn Cys Lys Gly		
485		

<210> 4  
 <211> 486  
 <212> PRT  
 <213> Bacillus subtilis  
 <400> 4

Met Ser Leu Phe Asp His Lys Ile Thr Glu Leu Lys Gln Leu Ile His
1 5 10 15
Lys Lys Glu Ile Lys Ile Ser Asp Leu Val Asp Glu Ser Tyr Lys Arg
20 25 30
Ile Gln Ala Val Asp Asp Lys Val Gln Ala Phe Leu Ala Leu Asp Glu
35 40 45
Glu Arg Ala Arg Ala Tyr Ala Lys Glu Leu Asp Glu Ala Val Asp Gly
50 55 60

1200029-US2.ST25.txt

Arg Ser Glu His Gly Leu Leu Phe Gly Met Pro Ile Gly Val Lys Asp  
65 70 75 80

Asn Ile Val Thr Lys Gly Leu Arg Thr Thr Cys Ser Ser Lys Ile Leu  
85 90 95

Glu Asn Phe Asp Pro Ile Tyr Asp Ala Thr Val Val Gln Arg Leu Gln  
100 105 110

Asp Ala Glu Ala Val Thr Ile Gly Lys Leu Asn Met Asp Glu Phe Ala  
115 120 125

Met Gly Ser Ser Thr Glu Asn Ser Ala Tyr Lys Leu Thr Lys Asn Pro  
130 135 140

Trp Asn Leu Asp Thr Val Pro Gly Gly Ser Ser Gly Gly Ser Ala Ala  
145 150 155 160

Ala Val Ala Ala Gly Glu Val Pro Phe Ser Leu Gly Ser Asp Thr Gly  
165 170 175

Gly Ser Ile Arg Gln Pro Ala Ser Phe Cys Gly Val Val Gly Leu Lys  
180 185 190

Pro Thr Tyr Gly Arg Val Ser Arg Tyr Gly Leu Val Ala Phe Ala Ser  
195 200 205

Ser Leu Asp Gln Ile Gly Pro Ile Thr Arg Thr Val Glu Asp Asn Ala  
210 215 220

Phe Leu Leu Gln Ala Ile Ser Gly Val Asp Lys Met Asp Ser Thr Ser  
225 230 235 240

Ala Asn Val Asp Val Pro Asp Phe Leu Ser Ser Leu Thr Gly Asp Ile  
245 250 255

Lys Gly Leu Lys Ile Ala Val Pro Lys Glu Tyr Leu Gly Glu Gly Val  
260 265 270

Gly Lys Glu Ala Arg Glu Ser Val Leu Ala Ala Leu Lys Val Leu Glu  
275 280 285

Gly Leu Gly Ala Thr Trp Glu Glu Val Ser Leu Pro His Ser Lys Tyr  
290 295 300

Ala Leu Ala Thr Tyr Tyr Leu Leu Ser Ser Ser Glu Ala Ser Ala Asn  
305 310 315 320

1200029-US2.ST25.txt

Leu Ala Arg Phe Asp Gly Ile Arg Tyr Gly Tyr Arg Thr Asp Asn Ala  
325 330 335

Asp Asn Leu Ile Asp Leu Tyr Lys Gln Thr Arg Ala Glu Gly Phe Gly  
340 345 350

Asn Glu Val Lys Arg Arg Ile Met Leu Gly Thr Phe Ala Leu Ser Ser  
355 360 365

Gly Tyr Tyr Asp Ala Tyr Tyr Lys Lys Ala Gln Lys Val Arg Thr Leu  
370 375 380

Ile Lys Lys Asp Phe Glu Asp Val Phe Glu Lys Tyr Asp Val Ile Val  
385 390 395 400

Gly Pro Thr Thr Pro Thr Pro Ala Phe Lys Ile Gly Glu Asn Thr Lys  
405 410 415

Asp Pro Leu Thr Met Tyr Ala Asn Asp Ile Leu Thr Ile Pro Val Asn  
420 425 430

Leu Ala Ala Tyr Arg Glu Ser Gly Ala Met Arg Leu Ala Asp Gly Leu  
435 440 445

Pro Leu Gly Leu Gln Ile Ile Gly Lys His Phe Asp Glu Ala Leu Tyr  
450 455 460

Thr Ala Leu Leu Met His Leu Asn Lys Gln Glu Thr Ile Ile Lys Gln  
465 470 475 480

Asn Leu Asn Cys Lys Gly  
485

<210> 5  
<211> 1431  
<212> DNA  
<213> Bacillus subtilis

<220>  
<221> CDS  
<222> (1)..(1428)  
<223> subunit B, corresponds to nucleotides 1876 - 3306 of SEQ ID NO: 1

<220>  
<221> misc\_feature  
<222> (152)..(152)  
<223> Xaa is Phe, Ser, Tyr, or Cys

<220>  
<221> misc\_feature

## 1200029-US2.ST25.txt

&lt;222&gt; (164)..(164)

&lt;223&gt; Xaa is Ser, Pro, Thr, or Ala

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (455)..(490)

&lt;223&gt; n is a, c, t, or g

&lt;400&gt; 5

ttg	aac	ttt	gaa	acg	gta	atc	gga	ctt	gaa	gtc	cac	ggt	gag	tta	aaa	48
Leu	Asn	Phe	Glu	Thr	Val	Ile	Gly	Leu	Glu	Val	His	Val	Glu	Leu	Lys	
1				5				10					15			

aca	aaa	tca	aaa	att	ttc	tca	agc	tct	cca	acg	cca	ttc	ggc	gcg	gag	96
Thr	Lys	Ser	Lys	Ile	Phe	Ser	Ser	Ser	Pro	Thr	Pro	Phe	Gly	Ala	Glu	
			20					25					30			

gcg	aat	acg	cag	aca	agc	gtt	att	gac	ctc	gga	tat	ccg	ggc	gtc	ctg	144
Ala	Asn	Thr	Gln	Thr	Ser	Val	Ile	Asp	Leu	Gly	Tyr	Pro	Gly	Val	Leu	
		35					40					45				

cct	gtt	ctg	aac	aaa	gaa	gcc	gtt	gaa	ttc	gca	atg	aaa	gcc	gct	atg	192
Pro	Val	Leu	Asn	Lys	Glu	Ala	Val	Glu	Phe	Ala	Met	Lys	Ala	Ala	Met	
	50					55					60					

gcg	ctc	aac	tgt	gag	atc	gca	acg	gat	acg	aag	ttt	gac	cgc	aaa	aac	240
Ala	Leu	Asn	Cys	Glu	Ile	Ala	Thr	Asp	Thr	Lys	Phe	Asp	Arg	Lys	Asn	
65				70					75					80		

tat	ttc	tat	cct	gac	aac	ccg	aaa	gcg	tat	cag	att	tct	caa	ttt	gat	288
Tyr	Phe	Tyr	Pro	Asp	Asn	Pro	Lys	Ala	Tyr	Gln	Ile	Ser	Gln	Phe	Asp	
				85				90						95		

aag	cca	atc	ggc	gaa	aac	ggc	tgg	atc	gaa	att	gaa	gtc	ggc	ggc	aaa	336
Lys	Pro	Ile	Gly	Glu	Asn	Gly	Trp	Ile	Glu	Ile	Glu	Val	Gly	Gly	Lys	
			100					105					110			

aca	aaa	cgc	atc	ggc	atc	acg	cgc	ctt	cat	ctt	gaa	gag	gat	gcc	gga	384
Thr	Lys	Arg	Ile	Gly	Ile	Thr	Arg	Leu	His	Leu	Glu	Glu	Asp	Ala	Gly	
		115					120					125				

aaa	ctg	acg	cat	acg	ggc	gac	ggc	tat	tct	ctt	gtt	gac	ttc	aac	cgt	432
Lys	Leu	Thr	His	Thr	Gly	Asp	Gly	Tyr	Ser	Leu	Val	Asp	Phe	Asn	Arg	
	130					135					140					

caa	gga	acg	ccg	ctt	gtt	gag	tnc	gta	tca	gag	ccg	gac	atc	cgc	acg	480
Gln	Gly	Thr	Pro	Leu	Val	Glu	Xaa	Val	Ser	Glu	Pro	Asp	Ile	Arg	Thr	
145					150					155					160	

ccg	gaa	gaa	ncg	tac	gca	tat	ctt	gaa	aag	ctg	aaa	tcc	atc	atc	caa	528
Pro	Glu	Glu	Xaa	Tyr	Ala	Tyr	Leu	Glu	Lys	Leu	Lys	Ser	Ile	Ile	Gln	
				165				170						175		

tat	aca	ggc	gtt	tct	gac	tgt	aaa	atg	gaa	gaa	ggc	tca	ctt	cgc	tgt	576
Tyr	Thr	Gly	Val	Ser	Asp	Cys	Lys	Met	Glu	Glu	Gly	Ser	Leu	Arg	Cys	
			180					185					190			

gac	gcc	aat	atc	tct	ctt	cgt	ccg	atc	ggc	caa	gag	gaa	ttc	ggc	aca	624
Asp	Ala	Asn	Ile	Ser	Leu	Arg	Pro	Ile	Gly	Gln	Glu	Glu	Phe	Gly	Thr	
		195					200					205				

aaa	aca	gaa	ttg	aaa	aac	ttg	aac	tcc	ttt	gcg	ttt	gtt	caa	aaa	ggc	672
Lys	Thr	Glu	Leu	Lys	Asn	Leu	Asn	Ser	Phe	Ala	Phe	Val	Gln	Lys	Gly	

1200029-US2.ST25.txt

210	215	220	
ctt gag cat gaa gaa aaa cgc cag gag cag gtt ctt ctt tcc ggc ttc Leu Glu His Glu Glu Lys Arg Gln Glu Gln Val Leu Leu Ser Gly Phe 225 230 235 240			720
ttc atc cag caa gaa act cgc cgt tat gat gaa gca acg aag aaa acc Phe Ile Gln Gln Glu Thr Arg Arg Tyr Asp Glu Ala Thr Lys Lys Thr 245 250 255			768
att ctt atg cgt gtc aaa gag gga tct gac gac tac cgt tac ttt cca Ile Leu Met Arg Val Lys Glu Gly Ser Asp Asp Tyr Arg Tyr Phe Pro 260 265 270			816
gag cca gat cta gtc gag ctc tac att gat gat gaa tgg aag gaa cgc Glu Pro Asp Leu Val Glu Leu Tyr Ile Asp Asp Glu Trp Lys Glu Arg 275 280 285			864
gta aaa gca agc att cct gag ctt ccg gat gag cgc cgc aag cgt tat Val Lys Ala Ser Ile Pro Glu Leu Pro Asp Glu Arg Arg Lys Arg Tyr 290 295 300			912
atc gaa gag ctt ggc ttc gct gca tat gac gca atg gtt ctg acg ctg Ile Glu Glu Leu Gly Phe Ala Ala Tyr Asp Ala Met Val Leu Thr Leu 305 310 315 320			960
aca aaa gaa atg gct gat ttc ttc gaa gaa acc gtt caa aaa ggc gct Thr Lys Glu Met Ala Asp Phe Phe Glu Glu Thr Val Gln Lys Gly Ala 325 330 335			1008
gaa gct aaa caa gcg tct aac tgg ctg atg ggt gaa gtg tca gct tac Glu Ala Lys Gln Ala Ser Asn Trp Leu Met Gly Glu Val Ser Ala Tyr 340 345 350			1056
cta aac gca gaa caa aaa gag ctt gcc gat gtt gcc ctg aca cct gaa Leu Asn Ala Glu Gln Lys Glu Leu Ala Asp Val Ala Leu Thr Pro Glu 355 360 365			1104
ggc ctt gcc ggc atg atc aaa ttg att gaa aaa gga acc att tct tct Gly Leu Ala Gly Met Ile Lys Leu Ile Glu Lys Gly Thr Ile Ser Ser 370 375 380			1152
aag atc gcg aag aaa gtg ttt aaa gaa ttg att gaa aaa ggc ggc gac Lys Ile Ala Lys Lys Val Phe Lys Glu Leu Ile Glu Lys Gly Gly Asp 385 390 395 400			1200
gct gag aag att gtg aaa gag aaa ggc ctt gtt cag att tct gac gaa Ala Glu Lys Ile Val Lys Glu Lys Gly Leu Val Gln Ile Ser Asp Glu 405 410 415			1248
ggc gtg ctt ctg aag ctt gtc act gag gcg ctt gac aac aat cct caa Gly Val Leu Leu Lys Leu Val Thr Glu Ala Leu Asp Asn Asn Pro Gln 420 425 430			1296
tca atc gaa gac ttt aaa aac gga aaa gac gcg atc ggc ttc cta Ser Ile Glu Asp Phe Lys Asn Gly Lys Asp Arg Ala Ile Gly Phe Leu 435 440 445			1344
gtc gga cag att atg aaa gcg tcc aaa gga caa gcc aac ccg ccg atg Val Gly Gln Ile Met Lys Ala Ser Lys Gly Gln Ala Asn Pro Pro Met 450 455 460			1392
gtc aac aaa att ctg ctt gaa gaa att aaa aaa cgc taa			1431

Val Asn Lys Ile Leu Leu Glu Glu Ile Lys Lys Arg  
 465 470 475

<210> 6  
 <211> 476  
 <212> PRT  
 <213> Bacillus subtilis

<220>  
 <221> MISC\_FEATURE  
 <222> (152)..(152)  
 <223> Xaa is Phe, Ser, Tyr, or Cys

<220>  
 <221> MISC\_FEATURE  
 <222> (164)..(164)  
 <223> Xaa is Ser, Pro, Thr, or Ala

<400> 6

Leu Asn Phe Glu Thr Val Ile Gly Leu Glu Val His Val Glu Leu Lys  
 1 5 10 15

Thr Lys Ser Lys Ile Phe Ser Ser Ser Pro Thr Pro Phe Gly Ala Glu  
 20 25 30

Ala Asn Thr Gln Thr Ser Val Ile Asp Leu Gly Tyr Pro Gly Val Leu  
 35 40 45

Pro Val Leu Asn Lys Glu Ala Val Glu Phe Ala Met Lys Ala Ala Met  
 50 55 60

Ala Leu Asn Cys Glu Ile Ala Thr Asp Thr Lys Phe Asp Arg Lys Asn  
 65 70 75 80

Tyr Phe Tyr Pro Asp Asn Pro Lys Ala Tyr Gln Ile Ser Gln Phe Asp  
 85 90 95

Lys Pro Ile Gly Glu Asn Gly Trp Ile Glu Ile Glu Val Gly Gly Lys  
 100 105 110

Thr Lys Arg Ile Gly Ile Thr Arg Leu His Leu Glu Glu Asp Ala Gly  
 115 120 125

Lys Leu Thr His Thr Gly Asp Gly Tyr Ser Leu Val Asp Phe Asn Arg  
 130 135 140

Gln Gly Thr Pro Leu Val Glu Xaa Val Ser Glu Pro Asp Ile Arg Thr  
 145 150 155 160

Pro Glu Glu Xaa Tyr Ala Tyr Leu Glu Lys Leu Lys Ser Ile Ile Gln  
 165 170 175

1200029-US2.ST25.txt

Tyr Thr Gly Val Ser Asp Cys Lys Met Glu Glu Gly Ser Leu Arg Cys  
 180 185 190  
 Asp Ala Asn Ile Ser Leu Arg Pro Ile Gly Gln Glu Glu Phe Gly Thr  
 195 200 205  
 Lys Thr Glu Leu Lys Asn Leu Asn Ser Phe Ala Phe Val Gln Lys Gly  
 210 215 220  
 Leu Glu His Glu Glu Lys Arg Gln Glu Gln Val Leu Leu Ser Gly Phe  
 225 230 235 240  
 Phe Ile Gln Gln Glu Thr Arg Arg Tyr Asp Glu Ala Thr Lys Lys Thr  
 245 250 255  
 Ile Leu Met Arg Val Lys Glu Gly Ser Asp Asp Tyr Arg Tyr Phe Pro  
 260 265 270  
 Glu Pro Asp Leu Val Glu Leu Tyr Ile Asp Asp Glu Trp Lys Glu Arg  
 275 280 285  
 Val Lys Ala Ser Ile Pro Glu Leu Pro Asp Glu Arg Arg Lys Arg Tyr  
 290 295 300  
 Ile Glu Glu Leu Gly Phe Ala Ala Tyr Asp Ala Met Val Leu Thr Leu  
 305 310 315 320  
 Thr Lys Glu Met Ala Asp Phe Phe Glu Glu Thr Val Gln Lys Gly Ala  
 325 330 335  
 Glu Ala Lys Gln Ala Ser Asn Trp Leu Met Gly Glu Val Ser Ala Tyr  
 340 345 350  
 Leu Asn Ala Glu Gln Lys Glu Leu Ala Asp Val Ala Leu Thr Pro Glu  
 355 360 365  
 Gly Leu Ala Gly Met Ile Lys Leu Ile Glu Lys Gly Thr Ile Ser Ser  
 370 375 380  
 Lys Ile Ala Lys Lys Val Phe Lys Glu Leu Ile Glu Lys Gly Gly Asp  
 385 390 395 400  
 Ala Glu Lys Ile Val Lys Glu Lys Gly Leu Val Gln Ile Ser Asp Glu  
 405 410 415  
 Gly Val Leu Leu Lys Leu Val Thr Glu Ala Leu Asp Asn Asn Pro Gln



1200029-US2.ST25.txt

420

425

430

Ser Ile Glu Asp Phe Lys Asn Gly Lys Asp Arg Ala Ile Gly Phe Leu  
435 440 445

Val Gly Gln Ile Met Lys Ala Ser Lys Gly Gln Ala Asn Pro Pro Met  
450 455 460

Val Asn Lys Ile Leu Leu Glu Glu Ile Lys Lys Arg  
465 470 475

<210> 7  
<211> 291  
<212> DNA  
<213> Bacillus subtilis

<220>  
<221> CDS  
<222> (1)..(288)  
<223> Subunit C, corresponds to nucleotides 103 - 393 of SEQ ID NO: 1

<400> 7  
atg tca cga att tca ata gaa gaa gta aag cac gtt gcg cac ctt gca 48  
Met Ser Arg Ile Ser Ile Glu Glu Val Lys His Val Ala His Leu Ala  
1 5 10 15  
aga ctt gcg att act gaa gaa gaa gca aaa atg ttc act gaa cag ctc 96  
Arg Leu Ala Ile Thr Glu Glu Glu Ala Lys Met Phe Thr Glu Gln Leu  
20 25 30  
gac agt atc att tca ttt gcc gag gag ctt aat gag gtt aac aca gac 144  
Asp Ser Ile Ile Ser Phe Ala Glu Glu Leu Asn Glu Val Asn Thr Asp  
35 40 45  
aat gtg gag cct aca act cac gtg ctg aaa atg aaa aat gtc atg aga 192  
Asn Val Glu Pro Thr Thr His Val Leu Lys Met Lys Asn Val Met Arg  
50 55 60  
gaa gat gaa gcg ggt aaa ggt ctt ccg gtt gag gat gtc atg aaa aat 240  
Glu Asp Glu Ala Gly Lys Gly Leu Pro Val Glu Asp Val Met Lys Asn  
65 70 75 80  
gcg cct gac cat aaa gac ggc tat att cgt gtg cca tca att ctg gac 288  
Ala Pro Asp His Lys Asp Gly Tyr Ile Arg Val Pro Ser Ile Leu Asp  
85 90 95  
taa 291

<210> 8  
<211> 96  
<212> PRT  
<213> Bacillus subtilis

<400> 8

Met Ser Arg Ile Ser Ile Glu Glu Val Lys His Val Ala His Leu Ala  
1 5 10 15

1200029-US2.ST25.txt

Arg Leu Ala Ile Thr Glu Glu Glu Ala Lys Met Phe Thr Glu Gln Leu  
20 25 30

Asp Ser Ile Ile Ser Phe Ala Glu Glu Leu Asn Glu Val Asn Thr Asp  
35 40 45

Asn Val Glu Pro Thr Thr His Val Leu Lys Met Lys Asn Val Met Arg  
50 55 60

Glu Asp Glu Ala Gly Lys Gly Leu Pro Val Glu Asp Val Met Lys Asn  
65 70 75 80

Ala Pro Asp His Lys Asp Gly Tyr Ile Arg Val Pro Ser Ile Leu Asp  
85 90 95